

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: LI, Yi and RUBEN, Steven M.
- (ii) TITLE OF INVENTION: HUMAN AMINE RECEPTOR POLYPEPTIDES
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN AND FOX, P.L.L.C.
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 - (C) CITY: WASHINGTON
 - (D) STATE: DC
 - (E) COUNTRY: UNITED STATES OF AMERICA
 - (F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/314,006
 - (B) FILING DATE: 19-MAY-1999
 - (C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/467,559
 - (B) FILING DATE: 06-JUN-1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: STEFFE, ERIC K
 - (B) REGISTRATION NUMBER: 36,688
 - (C) REFERENCE/DOCKET NUMBER: 1488.0840001/EKS/HCC
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(2) INFORMATION FOR SEQ ID NO:1:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
 (A) NAME/KEY: CDS
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(B) LOCATION: 252..1262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| CTAGAGCTAG CAGGAGTAAC TCTCATGGAA CCTTGAAAC CATTCTTCAA TTGAATTTC    | 60  |
| GGGCACATTT GAATCAGTAC CCAGGGGCAC TGTACTATGC TCCCAGCTGG ACCTTAGTTT  | 120 |
| CCTCCTCCTC GTTTCACCCT GTGAGTAATT AACAGACAAA ATTTTTTTTTT TTTTTTTTTT | 180 |
| TTTTTTTTTT TTTTGGCCCT CCAGTGGAGA AGGTGGCCAG TTCTCAGACA GAGGAAGAGT  | 240 |
| AGAAATCATA A ATG AGA GCT GTC TTC ATC CAA GGT GCT GAA GAG CAC CCT   | 290 |
| Met Arg Ala Val Phe Ile Gln Gly Ala Glu Glu His Pro                |     |
| 1 5 10                                                             |     |
| GCG GCA TTC TGC TAC CAG GTG AAT GGG TCT TGC CCC AGG ACA GTA CAT    | 338 |
| Ala Ala Phe Cys Tyr Gln Val Asn Gly Ser Cys Pro Arg Thr Val His    |     |
| 15 20 25                                                           |     |
| ACT CTG GGC ATC CAG TTG GTC ATC TAC CTG ACC TGT GCA GCA GGC ATG    | 386 |
| Thr Leu Gly Ile Gln Leu Val Ile Tyr Leu Thr Cys Ala Ala Gly Met    |     |
| 30 35 40 45                                                        |     |
| CTG ATT ATC GTG CTA GGG AAT GTA TTT GTG GCA TTT GCT GTG TCC TAC    | 434 |
| Leu Ile Ile Val Leu Gly Asn Val Phe Val Ala Phe Ala Val Ser Tyr    |     |
| 50 55 60                                                           |     |
| TTC AAA GCG CTT CAC ACG CCC ACC AAC TTC CTG CTG CTC TCC CTG GCC    | 482 |
| Phe Lys Ala Leu His Thr Pro Thr Asn Phe Leu Leu Leu Ser Leu Ala    |     |
| 65 70 75                                                           |     |
| CTG GCT GAC ATG TTT CTG GGT CTG CTG GTG CTG CCC CTC AGC ACC ATT    | 530 |
| Leu Ala Asp Met Phe Leu Gly Leu Leu Val Leu Pro Leu Ser Thr Ile    |     |
| 80 85 90                                                           |     |
| CGC TCA GTG GAG AGC TGC TGG TTC TTC GGG GAC TTC CTC TGC CGC CTG    | 578 |
| Arg Ser Val Glu Ser Cys Trp Phe Phe Gly Asp Phe Leu Cys Arg Leu    |     |
| 95 100 105                                                         |     |
| CAC ACC TAC CTG GAC ACC CTC TTC TGC CTC ACC TCC ATC TTC CAT CTC    | 626 |
| His Thr Tyr Leu Asp Thr Leu Phe Cys Leu Thr Ser Ile Phe His Leu    |     |
| 110 115 120 125                                                    |     |
| TGT TTC ATT TCC ATT GAC CGC CAC TGT GCC ATC TGT GAC CCC CTG CTC    | 674 |
| Cys Phe Ile Ser Ile Asp Arg His Cys Ala Ile Cys Asp Pro Leu Leu    |     |
| 130 135 140                                                        |     |
| TAT CCC TCC AAG TTC ACA GTG AGG GTG GCT CTC AGG TAC ATC CTG GCA    | 722 |
| Tyr Pro Ser Lys Phe Thr Val Arg Val Ala Leu Arg Tyr Ile Leu Ala    |     |
| 145 150 155                                                        |     |
| GGA TGG GGG GTG CCC GCA GCA TAC ACT TCG TTA TTC CTC TAC ACA GAT    | 770 |
| Gly Trp Gly Val Pro Ala Ala Tyr Thr Ser Leu Phe Leu Tyr Thr Asp    |     |
| 160 165 170                                                        |     |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| GTG GTA GAG ACA AGG CTC AGC CAG TGG CTG GAA GAG ATG CCT TGT GTG<br>Val Val Glu Thr Arg Leu Ser Gln Trp Leu Glu Glu Met Pro Cys Val<br>175 180 185     | 818  |
| GGC AGT TGC CAG CTG CTG CTC AAT AAA TTT TGG GGC TGG TTA AAC TTC<br>Gly Ser Cys Gln Leu Leu Leu Asn Lys Phe Trp Gly Trp Leu Asn Phe<br>190 195 200 205 | 866  |
| CCT TTG TTC TTT GTC CCC TGC CTC ATT ATG ATC AGC TTG TAT GTG AAG<br>Pro Leu Phe Phe Val Pro Cys Leu Ile Met Ile Ser Leu Tyr Val Lys<br>210 215 220     | 914  |
| ATC TTT GTG GTT GCT ACC AGA CAG GCT CAG CAG ATT ACC ACA TTG AGC<br>Ile Phe Val Val Ala Thr Arg Gln Ala Gln Gln Ile Thr Thr Leu Ser<br>225 230 235     | 962  |
| AAA AGC CTG GCT GGG GCT GCC AAG CAT GAG AGA AAA GCT GCC AAG ACC<br>Lys Ser Leu Ala Gly Ala Ala Lys His Glu Arg Lys Ala Ala Lys Thr<br>240 245 250     | 1010 |
| CTG GGC ATT GTT GTG GGC ATA TAC CTC TTG TGC TGG CTG CCC TTC ACC<br>Leu Gly Ile Val Val Gly Ile Tyr Leu Leu Cys Trp Leu Pro Phe Thr<br>255 260 265     | 1058 |
| ATA GAC ACG ATG GTC GAC AGC CTC CTT CAC TTT ATC ACA CCC CCA CTG<br>Ile Asp Thr Met Val Asp Ser Leu Leu His Phe Ile Thr Pro Pro Leu<br>270 275 280 285 | 1106 |
| GTC TTT GAC ATC TTT ATC TGG TTT GCT TAC TTC AAC TCA GCC TGC AAC<br>Val Phe Asp Ile Phe Ile Trp Phe Ala Tyr Phe Asn Ser Ala Cys Asn<br>290 295 300     | 1154 |
| CCC ATC ATC TAT GTC TTT TCC TAC CAG TGG TTT CGG AAG GCA CTG AAA<br>Pro Ile Ile Tyr Val Phe Ser Tyr Gln Trp Phe Arg Lys Ala Leu Lys<br>305 310 315     | 1202 |
| CTC ACA CTG AGC CAG AAG GTC TTC TCA CCG CAG ACA CGC ACT GTT GAT<br>Leu Thr Leu Ser Gln Lys Val Phe Ser Pro Gln Thr Arg Thr Val Asp<br>320 325 330     | 1250 |
| TTG TAC CAA GAA TGATTCCTTC TACTAAATGC AGGCAAGGAG TAGGACCTCA<br>Leu Tyr Gln Glu<br>335                                                                 | 1302 |
| CAGGAAAGAT AAGTGGCACT GTGACCGCGG GCTGTGTGGT GTTGAGTTTG TGGGCATGCT                                                                                     | 1362 |
| TCCAGGACAG CATGGGTT                                                                                                                                   | 1380 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Arg Ala Val Phe Ile Gln Gly Ala Glu Glu His Pro Ala Ala Phe
 1 5 10 15
Cys Tyr Gln Val Asn Gly Ser Cys Pro Arg Thr Val His Thr Leu Gly
 20 25 30
Ile Gln Leu Val Ile Tyr Leu Thr Cys Ala Ala Gly Met Leu Ile Ile
 35 40 45
Val Leu Gly Asn Val Phe Val Ala Phe Ala Val Ser Tyr Phe Lys Ala
 50 55 60
Leu His Thr Pro Thr Asn Phe Leu Leu Leu Ser Leu Ala Leu Ala Asp
 65 70 75 80
Met Phe Leu Gly Leu Leu Val Leu Pro Leu Ser Thr Ile Arg Ser Val
 85 90 95
Glu Ser Cys Trp Phe Phe Gly Asp Phe Leu Cys Arg Leu His Thr Tyr
 100 105 110
Leu Asp Thr Leu Phe Cys Leu Thr Ser Ile Phe His Leu Cys Phe Ile
 115 120 125
Ser Ile Asp Arg His Cys Ala Ile Cys Asp Pro Leu Leu Tyr Pro Ser
 130 135 140
Lys Phe Thr Val Arg Val Ala Leu Arg Tyr Ile Leu Ala Gly Trp Gly
 145 150 155 160
Val Pro Ala Ala Tyr Thr Ser Leu Phe Leu Tyr Thr Asp Val Val Glu
 165 170 175
Thr Arg Leu Ser Gln Trp Leu Glu Glu Met Pro Cys Val Gly Ser Cys
 180 185 190
Gln Leu Leu Leu Asn Lys Phe Trp Gly Trp Leu Asn Phe Pro Leu Phe
 195 200 205
Phe Val Pro Cys Leu Ile Met Ile Ser Leu Tyr Val Lys Ile Phe Val
 210 215 220
Val Ala Thr Arg Gln Ala Gln Gln Ile Thr Thr Leu Ser Lys Ser Leu
 225 230 235 240
Ala Gly Ala Ala Lys His Glu Arg Lys Ala Ala Lys Thr Leu Gly Ile
 245 250 255
Val Val Gly Ile Tyr Leu Leu Cys Trp Leu Pro Phe Thr Ile Asp Thr
 260 265 270
Met Val Asp Ser Leu Leu His Phe Ile Thr Pro Pro Leu Val Phe Asp
 275 280 285
Ile Phe Ile Trp Phe Ala Tyr Phe Asn Ser Ala Cys Asn Pro Ile Ile

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10021 54233550

290 295 300

Tyr Val Phe Ser Tyr Gln Trp Phe Arg Lys Ala Leu Lys Leu Thr Leu  
 305 310 315 320

Ser Gln Lys Val Phe Ser Pro Gln Thr Arg Thr Val Asp Leu Tyr Gln  
 325 330 335

Glu

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGGAATTCCT UATGAGAGCT GTCTTCATC

29

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGAAGCTTC GTCATTCTTG GTACAAATCA AC

32

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

T0027" 51288660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGGATCCCT CCATGAGAGC TGTCTTCATC

30

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGGGATCCCG CTCATTCTTG GTACAAATC

29

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTCCAAGCTT GCCACCATGA GAGCTGTCTT CATC

34

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTAGCTCGAG TCAAGCGTAG TCTGGGACGT CGTATGGGTA GCATTCTTGG TACAAATCAA

60

C

61

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

|            |            |            |            |          |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|----------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Ala<br>1   | Arg        | Leu        | Leu        | Val<br>5 | Leu        | Ala        | Ser        | Pro        | Pro<br>10  | Ala        | Ser        | Leu        | Leu        | Pro<br>15  | Pro        |
| Ala        | Ser        | Glu        | Gly<br>20  | Ser      | Ala        | Pro        | Leu        | Ser<br>25  | Gln        | Gln        | Trp        | Thr        | Ala<br>30  | Gly        | Met        |
| Gly        | Leu        | Leu        | Val<br>35  | Ala      | Leu        | Ile        | Val<br>40  | Leu        | Leu        | Ile        | Val        | Val<br>45  | Gly        | Asn        | Val        |
| Leu        | Val<br>50  | Ile        | Val        | Ala      | Ile        | Ala<br>55  | Lys        | Thr        | Pro        | Arg        | Leu<br>60  | Gln        | Thr        | Leu        | Thr        |
| Asn<br>65  | Leu        | Phe        | Ile        | Met      | Ser<br>70  | Leu        | Ala        | Ser        | Ala        | Asp<br>75  | Leu        | Val        | Met        | Gly        | Leu<br>80  |
| Leu        | Val        | Val        | Pro<br>85  | Phe      | Gly        | Ala        | Thr        | Ile        | Val<br>90  | Val        | Trp        | Gly        | Arg        | Trp<br>95  | Glu        |
| Tyr        | Gly        | Ser        | Phe<br>100 | Phe      | Cys        | Glu        | Leu        | Trp<br>105 | Thr        | Ser        | Val        | Asp        | Val<br>110 | Leu        | Cys        |
| Val        | Thr        | Ala<br>115 | Ser        | Ile      | Glu        | Thr        | Leu<br>120 | Cys        | Val        | Ile        | Ala        | Leu<br>125 | Asp        | Arg        | Tyr        |
| Leu        | Ala<br>130 | Ile        | Thr        | Ser      | Pro        | Phe<br>135 | Arg        | Tyr        | Gln        | Ser        | Leu<br>140 | Leu        | Thr        | Arg        | Ala        |
| Arg<br>145 | Ala        | Arg        | Ala        | Leu      | Val<br>150 | Cys        | Thr        | Val        | Trp        | Ala<br>155 | Ile        | Ser        | Ala        | Leu        | Val<br>160 |
| Ser        | Phe        | Leu        | Pro<br>165 | Ile      | Leu        | Met        | His        | Trp        | Trp<br>170 | Arg        | Ala        | Glu        | Ser        | Asp<br>175 | Glu        |
| Ala        | Arg        | Arg        | Cys<br>180 | Tyr      | Asn        | Asp        | Pro        | Lys<br>185 | Cys        | Cys        | Asp        | Phe        | Val<br>190 | Thr        | Asn        |
| Arg        | Ala        | Tyr<br>195 | Ala        | Ile      | Ala        | Ser        | Ser<br>200 | Val        | Val        | Ser        | Phe        | Tyr<br>205 | Val        | Pro        | Leu        |
| Cys        | Ile<br>210 | Met        | Ala        | Phe      | Val        | Tyr<br>215 | Leu        | Arg        | Val        | Phe        | Arg<br>220 | Glu        | Ala        | Gln        | Lys        |

Gln Val Lys Lys Ile Asp Ser Cys Glu Arg Arg Phe Leu Gly Gly Pro  
 225 230 235 240

Ala Arg Pro Pro Ser Pro Glu Pro Ser Pro Ser Pro Gly Pro Pro Arg  
 245 250 255

Pro Ala Asp Ser Leu Ala Asn Gly Arg Ser Ser Lys Arg Arg Pro Ser  
 260 265 270

Arg Leu Val Ala Leu Arg Glu Gln Lys Ala Leu Lys Thr Leu Gly Ile  
 275 280 285

Ile Met Gly Val Phe Thr Leu Cys Trp Leu Pro Phe Phe Leu Ala Asn  
 290 295 300

Val Val Lys Ala Phe His Arg Asp Leu Val Pro Asp Arg Leu Phe Val  
 305 310 315 320

Phe Phe Asn Trp Leu Gly Tyr Ala Asn Ser Ala Phe Asn Pro Ile Ile  
 325 330 335

Tyr Cys Arg Ser Pro Asp Phe Arg Lys Ala Phe Gln Arg Leu Leu Cys  
 340 345 350

Cys Ala Arg Arg Ala Ala Cys Arg Arg Arg Ala Ala His  
 355 360 365

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Asp Asp Asp Leu Glu Arg Gln Asn Trp Ser Arg Pro Phe Asn Gly Ser  
 1 5 10 15

Asp Gly Lys Ala Asp Arg Pro His Tyr Asn Tyr Tyr Ala Thr Leu Leu  
 20 25 30

Thr Leu Leu Ile Ala Val Ile Val Phe Gly Asn Val Leu Val Cys Met  
 35 40 45

Ala Val Ser Arg Glu Lys Ala Leu Gln Thr Thr Thr Asn Tyr Leu Ile  
 50 55 60

Val Ser Leu Ala Val Ala Asp Leu Leu Val Ala Thr Leu Val Met Pro  
 65 70 75 80

FOOTNOTES



Leu